Supplementary Information

Selective Targeting of SH2 Domain-Phosphotyrosine Interactions of Src Family Tyrosine Kinases with Monobodies

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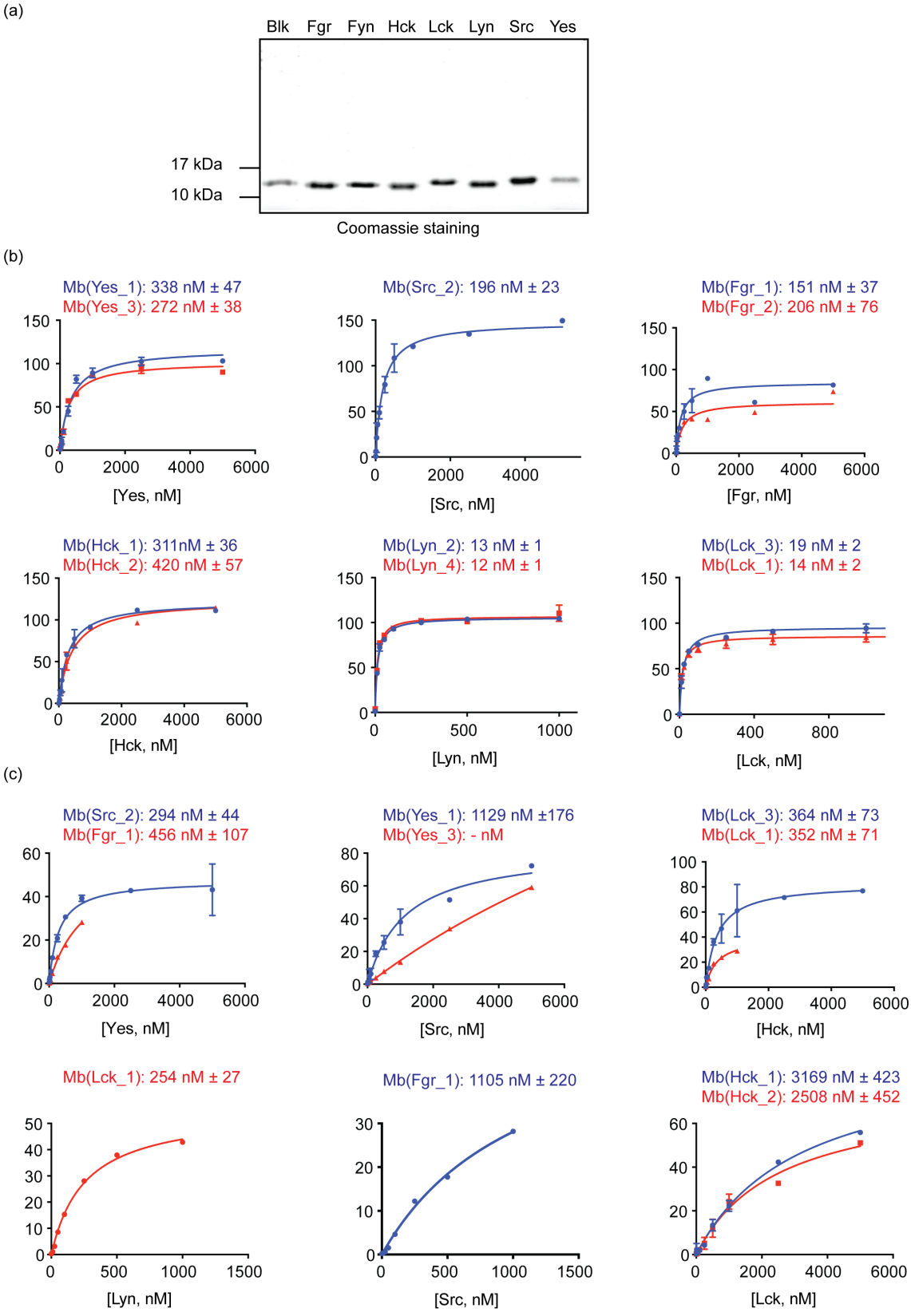
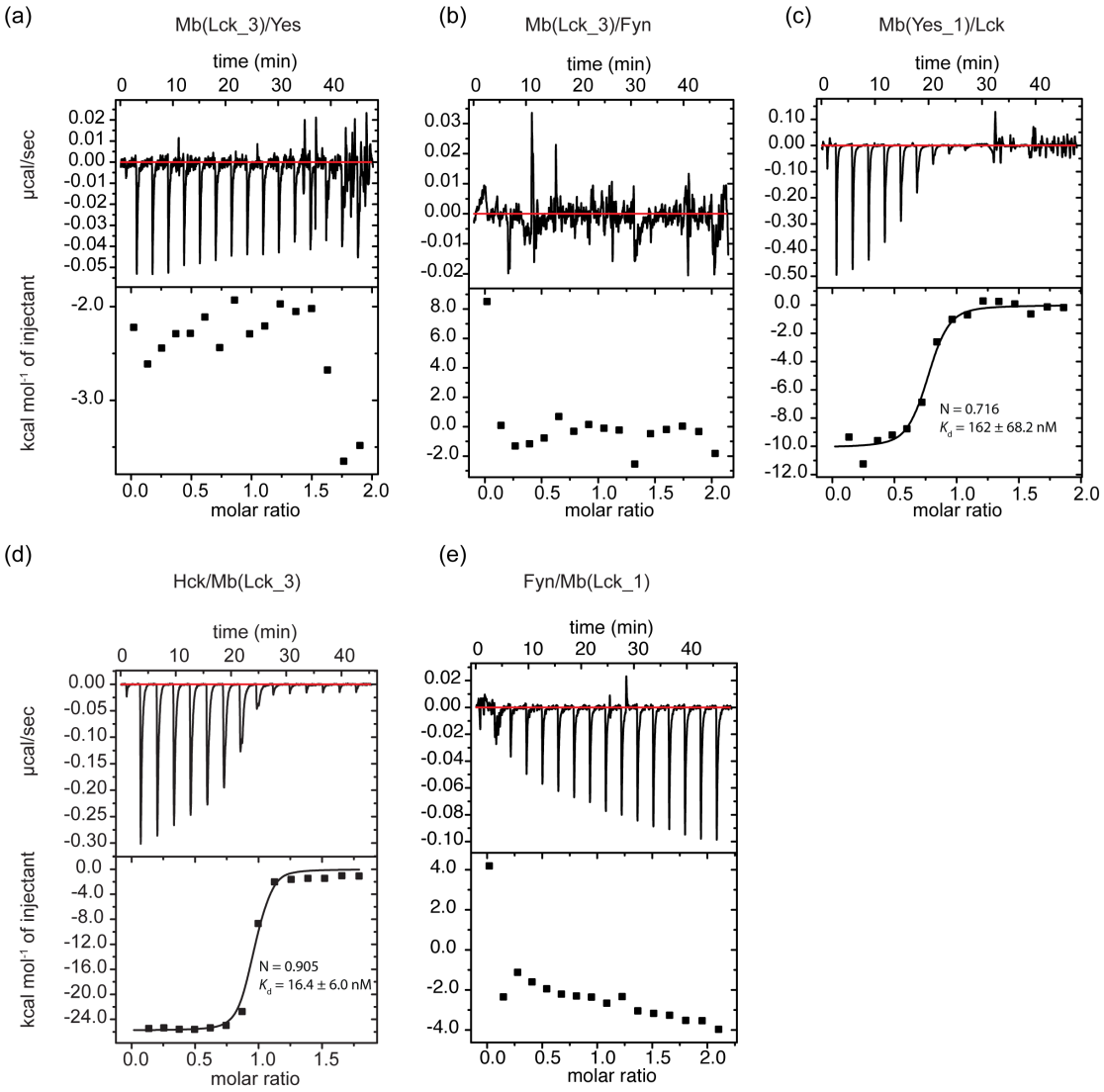
Content

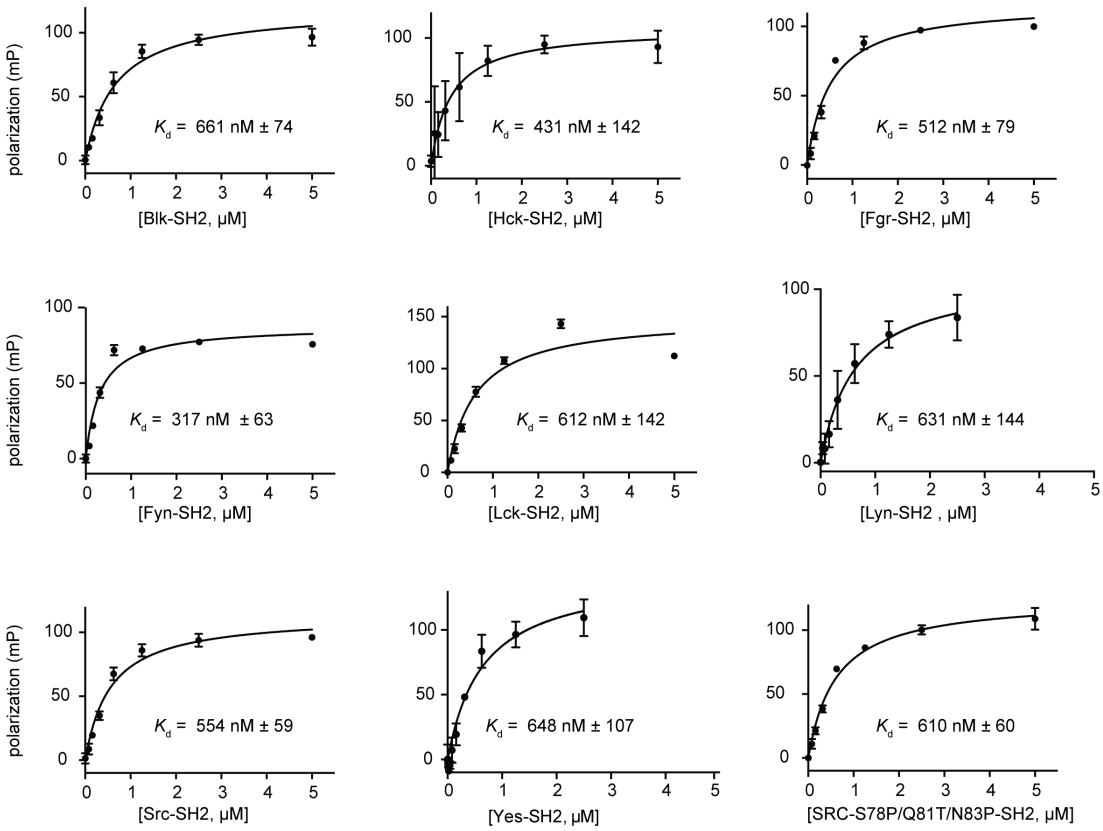
Supplementary Figures 1-10



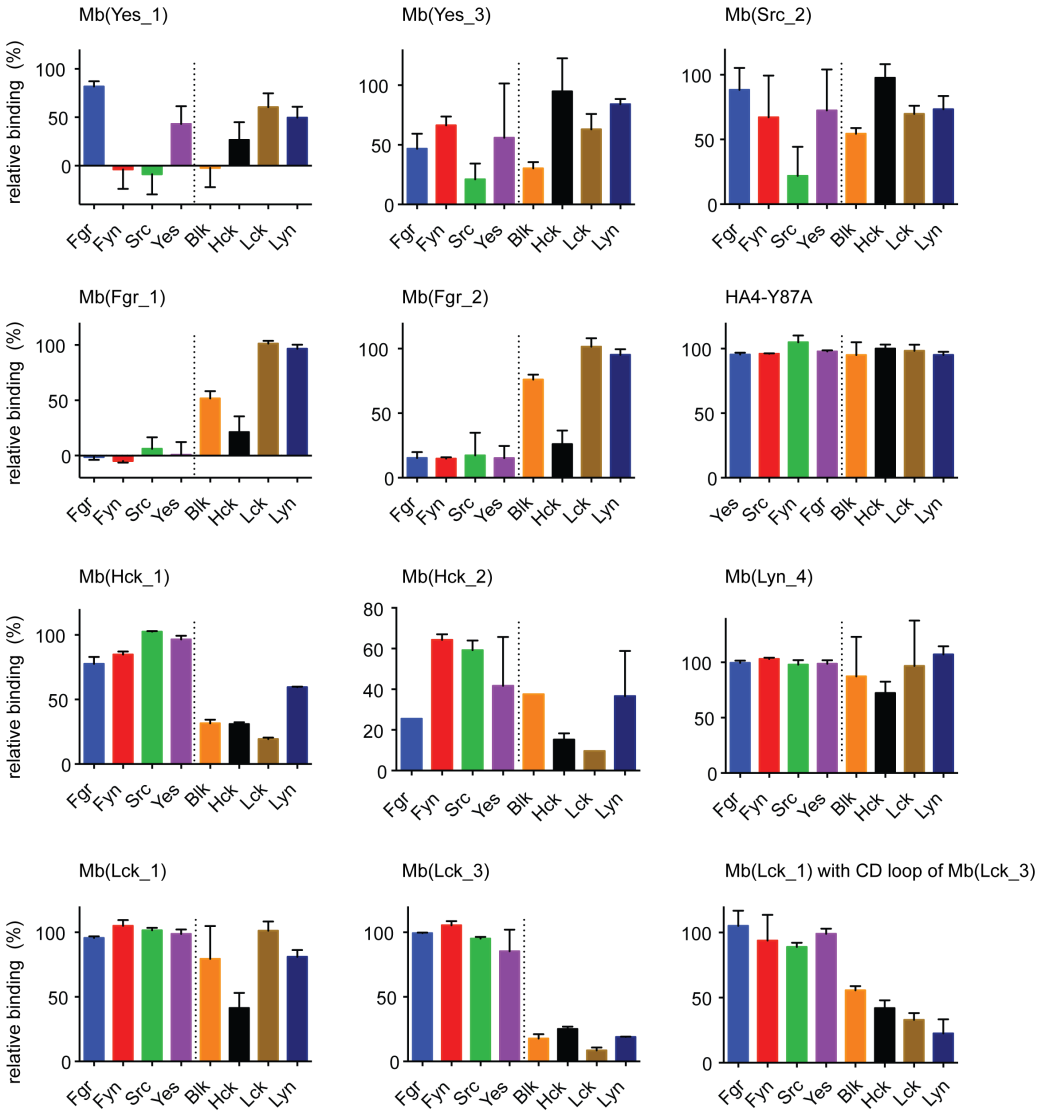
SI Figure 1: Target quality and affinity of binding clones. (a) Coomassie stained SDS-PAGE gel of 15 µL purified SH2 SFK domains at 15 µM concentration. All SFK SH2 domains have a calculated molecular weight of 13-14 kDa. These SH2 domains have been cleaved by TEV-protease and hence do not contain the 6xHis-Avi tags any more. A sequences alignment of all SFK SH2 domains used on this study is shown in SI Fig. 8. (b) Binding measurements by yeast surface display of representative monobodies used on this study. The mean fluorescence intensities of yeast cells displaying a monobody are plotted as a function of the concentration of the target. The errors indicated are the standard deviations from curve fitting of the 1:1 binding model. The derived K_d values from these graphs are reported in Fig. 1. Binding curves of monobody displaying yeast cells at different concentrations for their on-target and (c) monobody displaying yeast cell binding to other (off-target) Src family kinases SH2 domains.



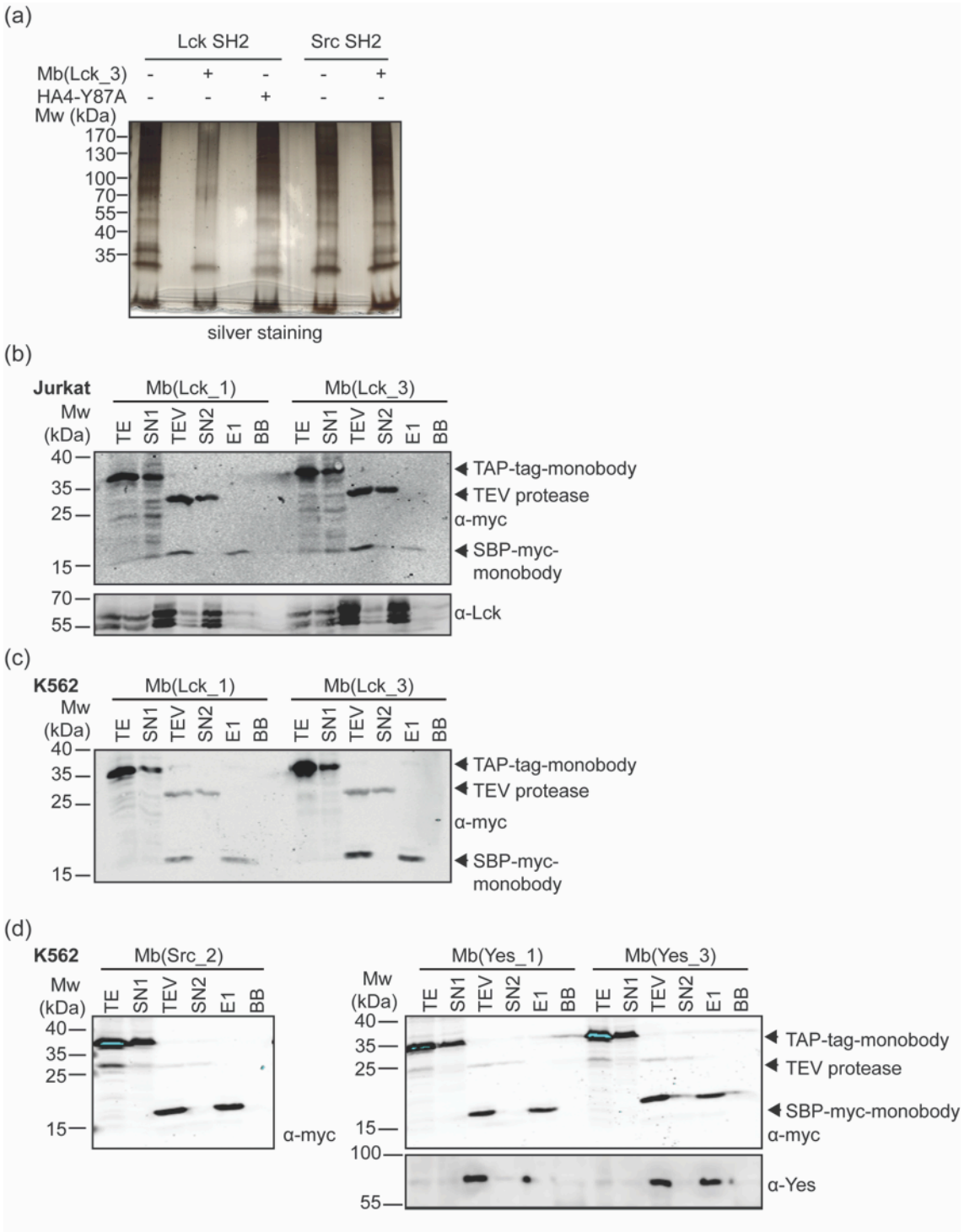
SI Figure 2: Isothermal titration calorimetry of monobody/SH2 interactions (upper panels) and fitted isotherms data of integrated peaks (lower panel) are shown for representative experiments. Labels show titration direction (first named in syringe and second in cell) and thermodynamic data of the fit generated by the MicroCal evaluation software. (a) Mb(Lck_3) (140 µM) titrated to Yes SH2 domain (15 µM), (b) Mb(Lck_3) (150 µM) titrated to Fyn SH2 domain (15 µM), (c) Mb(Yes_1) (400 µM) titrated to Lck SH2 domain (40 µM), (d) Hck SH2 domain (95 µM) titrated to Mb(Lck_3) (10 µM), (e) Fyn SH2 (176 µM) titrated to Mb(Lck_1) (17 µM). All experiments have been conducted at 25°C.



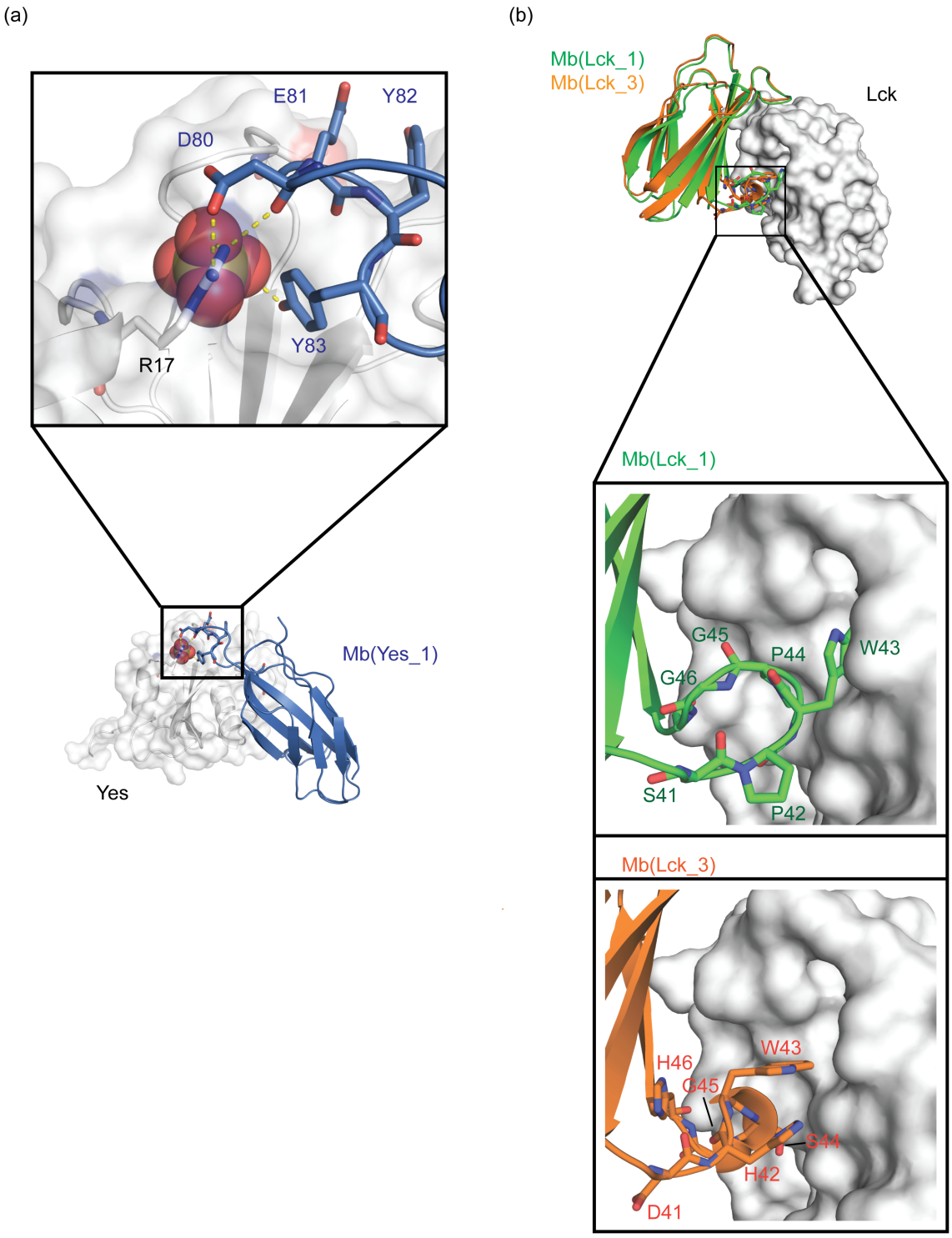
SI Figure 3: Fluorescence polarization assay of SFK SH2 domains and FITC-labeled pYEEI peptide**.** 250 nM (final concentration) of the pYEEI peptide were mixed with the indicated concentrations of recombinant SH2 domain of all eight Src family kinases as well as the mutant SRC-S78P/Q81T/N83P (see Fig. 7) to measure binding. All K_d values are shown in the graphs and have been fitted based on a 1:1 binding model (one-site specific binding, Prism).



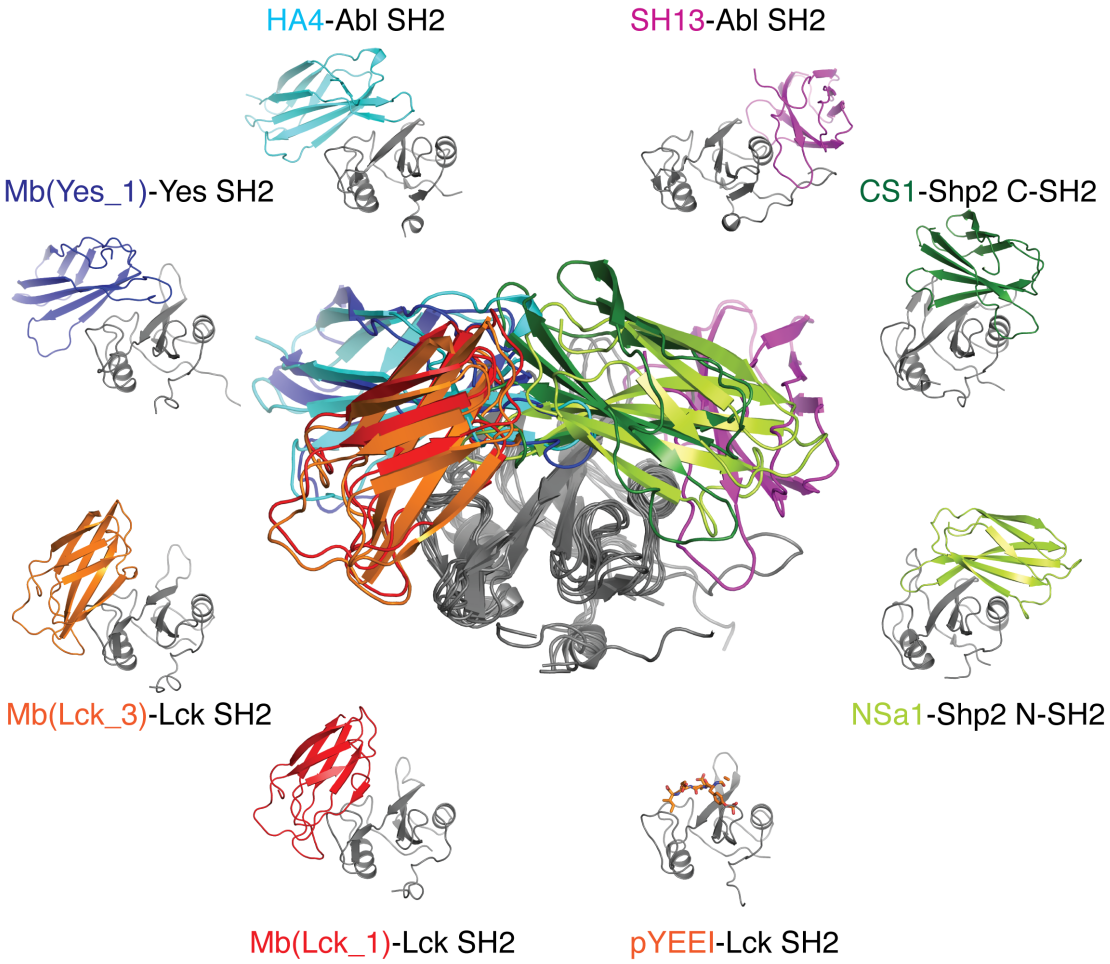
SI Figure 4: Inhibition of pYEEI peptide/SH2 interaction by monobodies in a fluorescence polarization assay. The graph shows relative pYEEI peptide binding (in %) to the SH2 domains (2.5 µM) in the presence of the indicated monobody (in 5-fold excess, i.e. 12.5 µM). In the lower right panel, a designed monobody, which is a chimeric variant of Mb(Lck_1) and Mb(Lck_3) has also been tested. This monobody contains the FG loop of Mb(Lck_1) and the CD loop of Mb(Lck_3). Further experiments with this chimeric monobody are shown in Figure 7. All eight SH2 domains have been measured without (see Fig. S3) and in the presence of the monobody selected for the respective on-target (see Fig. 4 a-b). The pYEEI peptide in isolation and SH2/pYEEI complex were set to 0% and 100% binding, respectively. Accordingly the reduction in binding observed with a monobody is expressed as a percentage of relative binding. Each datapoint corresponds to the average of at least two repeats +/- SD.


(a)
Lck SH2
Src SH2
Mb(Lck_3) - + - - +
HA4-Y87A - - + - -
Mw (kDa)
170
130
100
70
55
40
35
silver staining
(b)
Jurkat
Mb(Lck_1)
Mb(Lck_3)
Mw (kDa)
TE SN1 TEV SN2 E1 BB
40
35
25
15
70
55
TAP-tag-monobody
TEV protease
α-myc
SBP-myc-monobody
α-Lck
(c)
K562
Mb(Lck_1)
Mb(Lck_3)
Mw (kDa)
TE SN1 TEV SN2 E1 BB
40
35
25
15
TAP-tag-monobody
TEV protease
α-myc
SBP-myc-monobody
(d)
K562
Mb(Src_2)
Mb(Yes_1)
Mb(Yes_3)
Mw (kDa)
TE SN1 TEV SN2 E1 BB
40
35
25
15
100
55
α-myc
TAP-tag-monobody
TEV protease
SBP-myc-monobody
α-myc
α-Yes

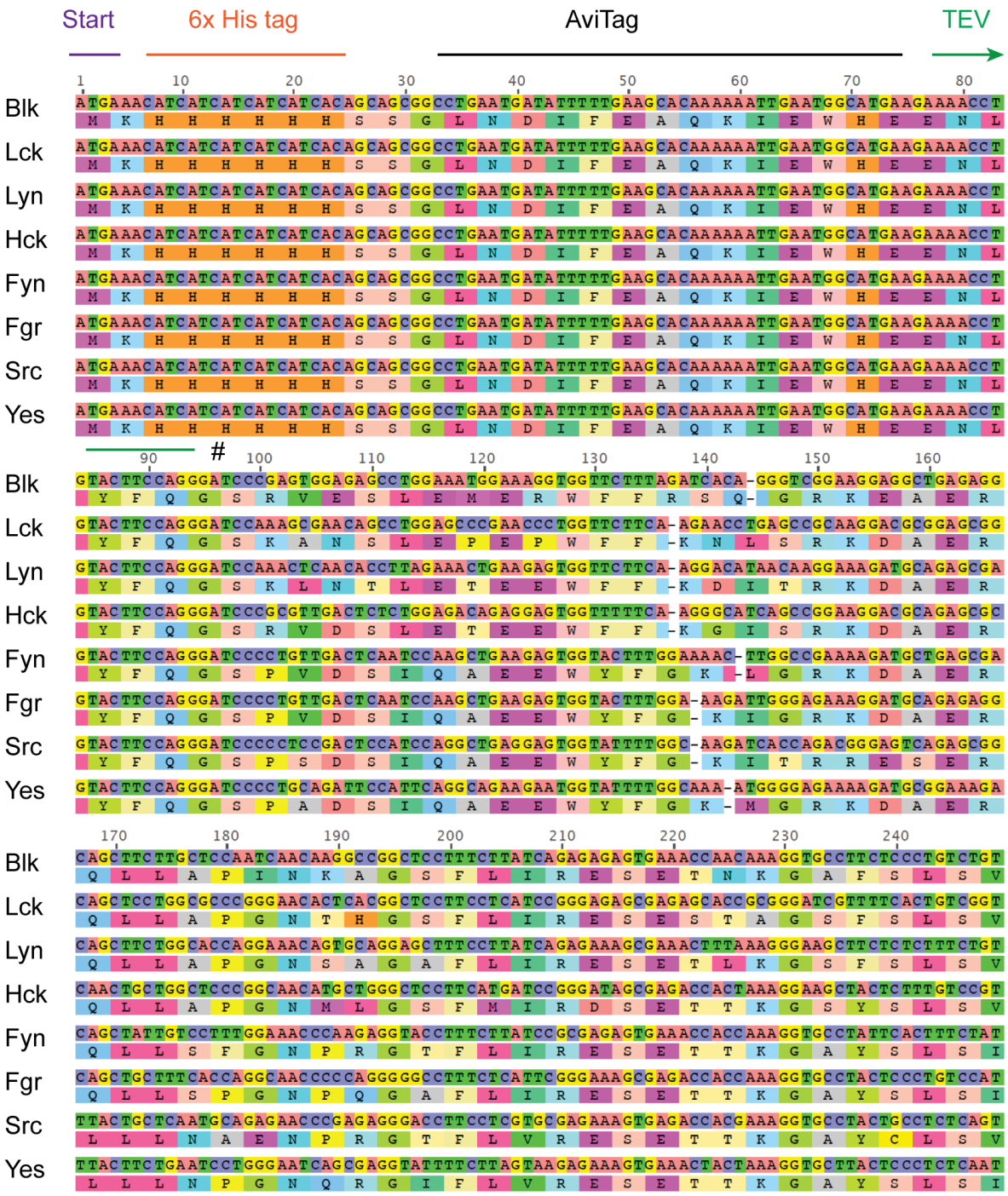
SI Figure 5: Mb(Lck_3) blocks the binding of Lck SH2 domain to interactors in cell lysates. (a) 10% fraction of beads after SH2 pull-down, separated by SDS/PAGE and visualized with silver staining. (b-d) SFK SH2 domain targeting monobodies bind their main target in cells. (b) Immunoblot analysis of TAP of Mb(Lck_1) and Mb(Lck_3) monobody complexes from Jurkat cells (see Fig. 5d). TE, total extract; SN1, supernatant IgG beads; TEV, eluate after TEV cleavage; SN2, supernatant streptavidin beads; E1, eluate from streptavidin beads; BB, boiled streptavidin beads to control the efficiency of elution. The bait protein as well as the main target of the monobodies were identified by immunoblotting using an anti-Myc or Lck antibody, respectively. (c) Immunoblot analysis of (Mb(Lck_1) and Mb(Lck_3) monobody from K562 (Abbreviations as in (a)). (d) Immunoblot analysis of TAP of Mb(Src_2), Mb(Yes_1) and Mb(Yes_3) monobody complexes from K562 cells (see Fig. 5c). The bait protein as well as the main target Yes were identified by immunoblotting using an anti-Myc or Yes antibody, respectively.



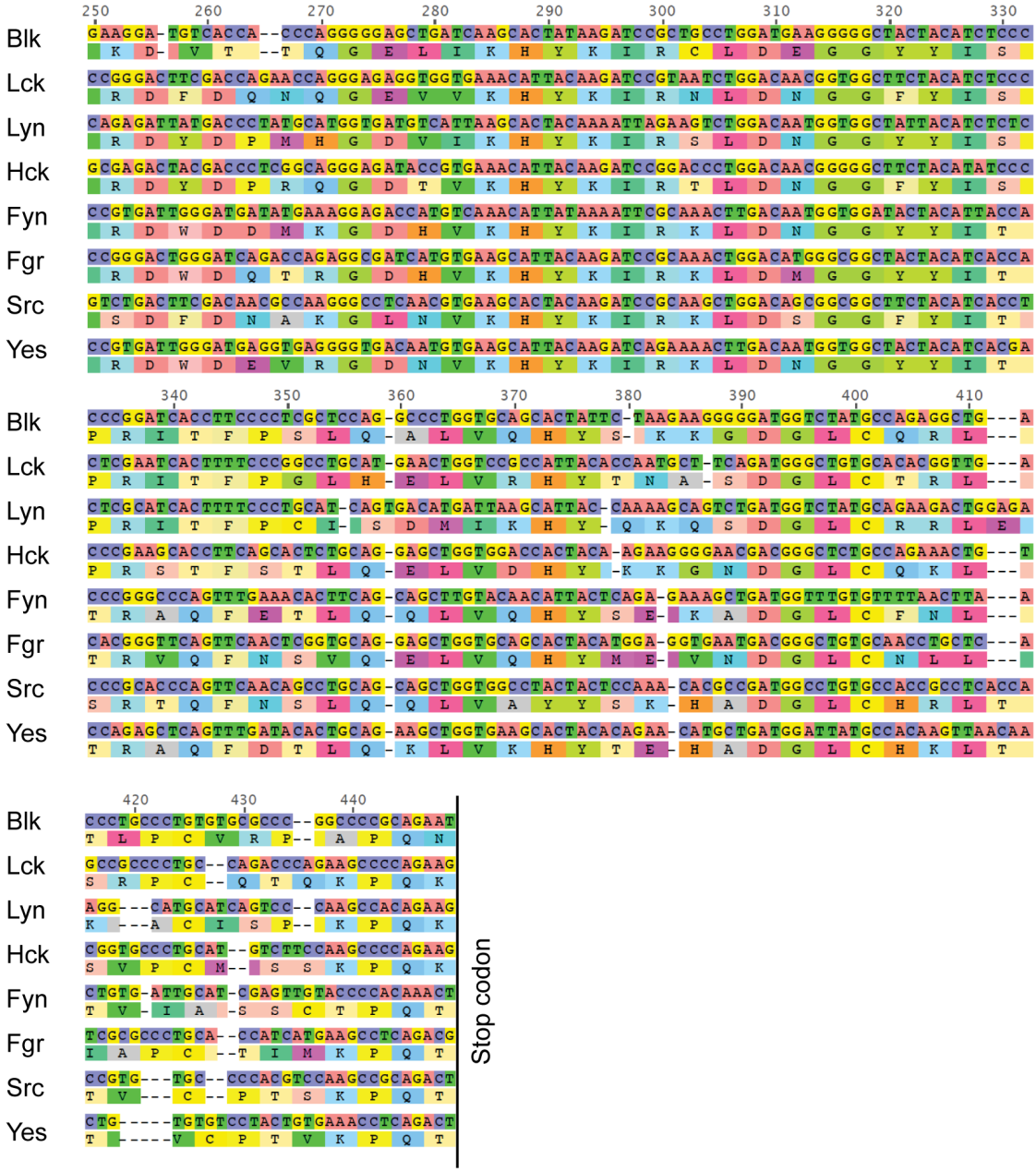
SI Figure 6: Monobody/SH2 – Structures. (a) Detailed view of Mb(Yes_1) binding to Yes SH2 domains showing the residues of the monobody FG loop involved to block the pY pocket of the SH2 domain (presented as blue sticks). A sulphate that was found in the pY pocket is shown as spheres. Hydrogen bonds are depicted as yellow dashed lines. (b) Overview of Mb(Lck_1) compared to Mb(Lck_3) binding to the Lck SH2 domain (overlay, top picture). The close-up shows the diversified residues of the monobody CD loops (presented as sticks) for Mb(Lck_1) (green, middle panel) and for Mb(Lck_3) (orange, lower panel) binding to the +3 specificity pocket of the Lck SH2 domain.



SI Figure 7: Structures of monobodies targeting different SH2 domains. Seven individual co-crystal structures of monobodies targeting SH2 domains (three structures reported in this study and four from previous studies) as well as the pYEEI peptide/Lck complex are shown. The SH2 domains are depicted in white whereas the monobodies and the pYEEI peptide are shown in different colors. The model in the center is a superimposition of all structures aligned to one SH2 domain. PDB entries used were: 3K2M (HA4-Abl SH2), 3UYO (SH13-Abl SH2), 4JE4 (NSa1-Shp2 N-SH2), 4JEG (CS1-Shp2 C-SH2) and 1LKK (pYEEI peptide-Lck SH2).



Sequences continue on next page

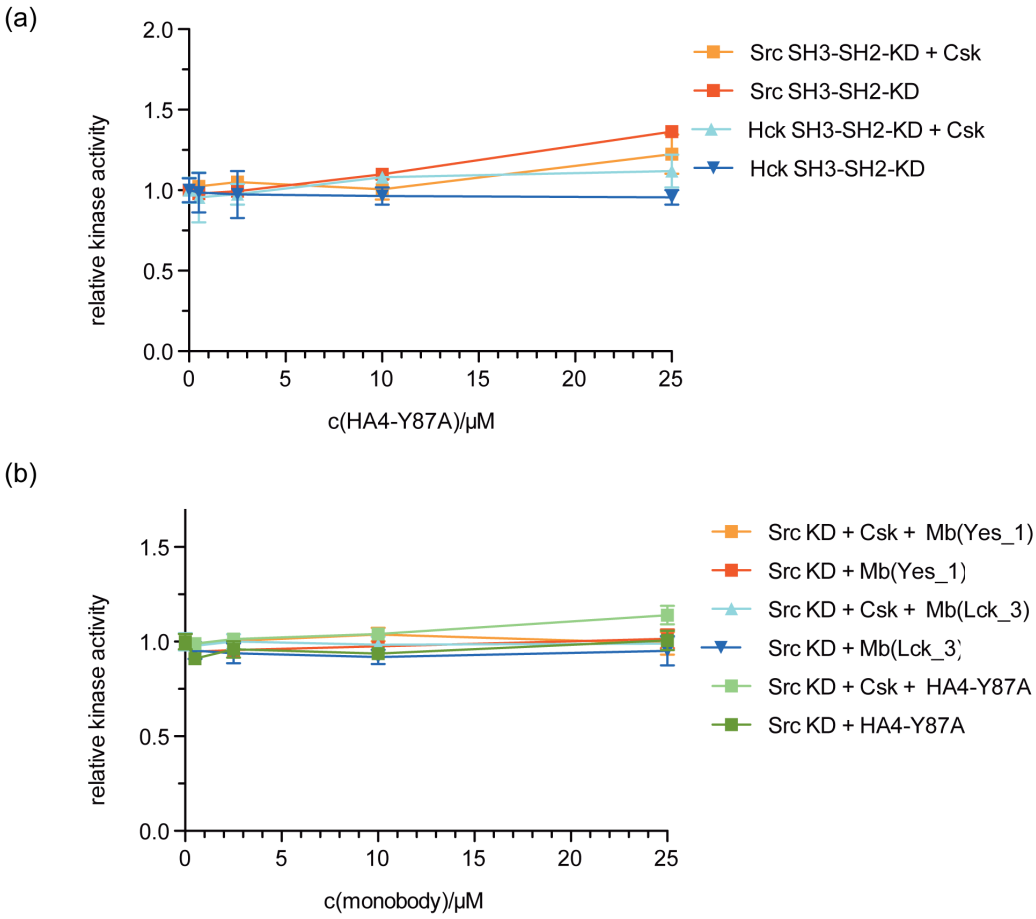


#: BamHI restriction site

SI Figure 8: Alignment of DNA and protein sequences of the SFK SH2 constructs used in our study. The sequences show the expressed protein/mRNA from the pHBT vector including 6xHis tag, AviTag, TEV cleavage site and SH2 sequence until the Stop codon. The alignment has been created with Geneious™ using a standard color scheme of the software. Each amino acid has a different color background in order to make sequence comparison easier.

* residues which have been mutated in our study.

SI Figure 9: Protein sequence alignment of all SFK SH2 domains used in this study. Vertical bars mark the sequence of the FLVRES motif (with a critical Arg residue for pY binding) and the EF-loop (contacted by the FG-loops of Mb(Lck_1) and Mb(Lck_3); see Fig. 7). The conservation of the residues at each position is visualized by a scale from black (high conservation) to white (low conservation).



SI Figure 10: Control experiments for the kinase activity assays of Fig.8. *In vitro* kinase activity of Src and Hck was measured in the absence or presence of Csk and set to 1.0. (a) Relative changes in kinase activity are shown at the indicated concentrations of monobody HA4-Y87A. (b) Effect of monobodies Mb(Yes_1) and Mb(Lck_3) on the relative kinase activity of the Src kinase domain (Src KD). The preparations of the Src KD proteins used in these assays displayed robust kinase activities with k_{cat}=60-80 min^{-1}. Each datapoint corresponds to the average of three repeats +/- SD.

Supplementary Information Tables SI 1-3

SI Table 1: Total spectrum counts of the proteins identified by mass spectrometry following tandem affinity purification of stable K562 cell lines expressing the bait proteins Mb(Src_2), Mb(Yes_1) or Mb(Yes_3).

Scaffold: Version: Scaffold_4.4.5
Modification Metadata Set: 1541 modifications
Source: C:\Program Files (x86)\Scaffold 4\parameters\unimod.xml
Comment:
Protein Grouping Strategy: Experiment-wide grouping with binary peptide-protein weights
Peptide Thresholds: 95.0% minimum
Protein Thresholds: 99.0% minimum and 2 peptides minimum
Peptide FDR: 0.0% (Decoy)
Protein FDR: 0.7% (Decoy)
GO Annotation Source(s):
Displaying: Total Spectrum Count

Identified Proteins (269)	Accession Number	Molecular Weight	Protein Grouping Ambiguity	K562 Mb(Src_2)	K562 Mb(Yes_1)	K562 Mb(Yes_3)
Non-specific protein-tyrosine kinase OS=Homo sapiens GN=YES1 PE=1 SV=1	J3QRU1 (+1)	61 kDa	TRUE	31	101	295
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	P04264	66 kDa	TRUE	152	142	228
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	P07900 (+1)	85 kDa	TRUE	0	43	217
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	P08238	83 kDa	TRUE	0	37	214
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	P11142	71 kDa	TRUE	46	26	158
Tyrosine-protein kinase Fyn OS=Homo sapiens GN=FYN PE=1 SV=3	P06241	61 kDa	TRUE	31	76	139
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	P13645	59 kDa	TRUE	84	103	137
Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	P38646	74 kDa	TRUE	26	26	133
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	P35527	62 kDa	TRUE	76	103	130
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	P35908	65 kDa	TRUE	99	89	126
Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens GN=SRC PE=1 SV=3	P12931 (+1)	60 kDa	TRUE	35	61	107
Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	P08779	51 kDa	TRUE	28	44	99
Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	P02533	52 kDa	TRUE	37	55	90
Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1	B4DV12 (+13)	17 kDa		6	5	73
Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	P04259	60 kDa	TRUE	0	0	70
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	P11021	72 kDa	TRUE	23	13	61
Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	P02538	60 kDa	TRUE	16	22	59
Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3	P48668	60 kDa	TRUE	15	22	55
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	P07437	50 kDa	TRUE	10	19	50
Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	P98160	469 kDa		0	0	48
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	P68371	50 kDa	TRUE	0	0	47
Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	P08107	?	TRUE	15	10	45
Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	Q04695	48 kDa	TRUE	0	0	44
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	P13647	62 kDa	TRUE	13	11	41
DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	P78527	469 kDa		0	0	39
Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2	P34931	70 kDa	TRUE	0	0	38
Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	Q71U36	50 kDa	TRUE	3	10	37
Isoform 2 of Tyrosine-protein kinase Lyn OS=Homo sapiens GN=LYN	P07948-2	56 kDa	TRUE	0	12	32
Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	Q16543	44 kDa	TRUE	0	11	30
Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=1	A0A087WUZ3 (+1)	275 kDa	TRUE	0	0	30
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Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	P15924	332 kDa		0	0	20
CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1	F8VPD4 (+1)	236 kDa	TRUE	0	0	20
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	Q9Y490	270 kDa	TRUE	0	0	19
Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1	A0A0C4DGB6 (+2)	69 kDa		2	0	18
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	P60709 (+1)	42 kDa		0	0	17
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=1	E9PL09 (+2)	25 kDa		8	15	16
Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Homo sapiens GN=FKBP5 PE=1 SV=2	Q13451	51 kDa		0	6	16
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	P61978 (+2)	51 kDa		2	5	16
Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	Q7Z794	62 kDa	TRUE	19	0	16
Isoform 3 of Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA	Q13085-3	257 kDa	TRUE	0	0	16
Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	P08727	44 kDa	TRUE	0	3	15
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1	Q9HCC0 (+1)	61 kDa		0	0	15
Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	P34932	94 kDa	TRUE	0	0	14
Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	Q5T749	64 kDa		0	2	13
ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	P25705	60 kDa		2	0	13
Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	P05787 (+1)	54 kDa	TRUE	0	0	13
Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	Q9BUF5	50 kDa	TRUE	0	0	13
Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	Q5XKE5	58 kDa	TRUE	0	0	13
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	P49327	273 kDa		0	0	12
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	P02751 (+13)	263 kDa	TRUE	19	0	11
Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	O14980	123 kDa		1	0	11
T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	P50990	60 kDa		0	3	10
Tyrosine-protein kinase ABL1 OS=Homo sapiens GN=ABL1 PE=1 SV=4	P00519 (+1)	123 kDa	TRUE	0	0	10
Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	P40939	83 kDa		0	0	10
Keratin, type I cuticular Ha6 OS=Homo sapiens GN=KRT36 PE=2 SV=1	O76013	52 kDa	TRUE	0	0	10
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	P55072	89 kDa	TRUE	0	0	10
RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	H3BPE7 (+2)	53 kDa		1	1	9
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	P68104 (+1)	50 kDa		1	0	9
Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	Q02413	114 kDa		0	0	9
T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	P17987	60 kDa	TRUE	0	0	9
Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	P07814	171 kDa		0	0	9
Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=2	Q92734 (+1)	43 kDa		0	0	9
Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3	Q14315 (+1)	291 kDa	TRUE	0	0	9
E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	Q7Z6Z7 (+2)	482 kDa		0	0	8
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	P14923	82 kDa		0	0	8
T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1	B4DUR8 (+2)	56 kDa		0	0	7
T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	Q99832 (+1)	59 kDa		0	0	7
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	P13639	95 kDa	TRUE	0	0	7
Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3	P55084 (+1)	51 kDa		0	0	7
Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	P06702	13 kDa		0	0	7
Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	Q8N1N4	57 kDa	TRUE	0	0	7
DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	Q16531	127 kDa		0	1	6
Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	Q01469	15 kDa		1	0	6
Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1	O95831 (+1)	67 kDa		0	0	6
Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3	O95757	95 kDa	TRUE	0	0	6
D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	O43175	57 kDa		0	0	6
Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	P07355	39 kDa		0	0	6
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	P50991	58 kDa	TRUE	0	0	6
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	Q09666	629 kDa		0	0	6
Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=2 SV=2	Q9NSB2	65 kDa	TRUE	0	0	6
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Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	P19338	77 kDa		0	0	6
Zinc finger protein 598 OS=Homo sapiens GN=ZNF598 PE=1 SV=1	Q86UK7 (+2)	99 kDa		0	0	6
General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2	O60763 (+1)	108 kDa		0	0	6
Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	Q92616	293 kDa		0	0	5
Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens GN=SNRPB PE=1 SV=3	A8MT02 (+3)	30 kDa		0	0	5
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=1	B0YJC4 (+1)	50 kDa	TRUE	0	0	5
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	P16615 (+3)	115 kDa		0	0	5
Polyadenylate-binding protein OS=Homo sapiens GN=PABPC4 PE=1 SV=1	B1ANR0 (+3)	68 kDa	TRUE	0	0	5
Keratin, type I cuticular Ha1 OS=Homo sapiens GN=KRT31 PE=1 SV=3	Q15323	47 kDa	TRUE	0	0	5
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	P06733	47 kDa		0	0	5
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	Q14974	97 kDa		0	0	5
Galactocerebrosidase OS=Homo sapiens GN=GALC PE=1 SV=1	A0A0A0MQV0 (+1)	77 kDa		0	0	5
Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1	H3BLZ8 (+4)	80 kDa	TRUE	0	0	5
Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	P29508 (+1)	45 kDa		0	0	5
4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=1	F5GZS6 (+5)	65 kDa		0	0	5
AH receptor-interacting protein OS=Homo sapiens GN=AIP PE=1 SV=2	O00170	38 kDa		0	0	5
Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	O43143	91 kDa		0	0	5
Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2	Q15437	86 kDa		0	0	5
Polyadenylate-binding protein OS=Homo sapiens GN=PABPC1 PE=1 SV=1	A0A087WTT1 (+3)	59 kDa	TRUE	0	0	5
Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	Q13263	89 kDa		0	2	4
U1 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA PE=1 SV=3	P09012	31 kDa		1	1	4
Tyrosine-protein kinase BTK OS=Homo sapiens GN=BTK PE=1 SV=3	Q06187 (+1)	76 kDa		0	1	4
Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	Q9NZT1	16 kDa		1	0	4
Peroxiredoxin-1 (Fragment) OS=Homo sapiens GN=PRDX1 PE=1 SV=1	A0A0A0MSI0 (+1)	19 kDa	TRUE	1	0	4
Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	P42704	158 kDa		1	0	4
Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	Q13835	83 kDa		0	0	4
Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1	Q92598 (+1)	97 kDa	TRUE	0	0	4
Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	P04040	60 kDa		0	0	4
Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=1	A0A087X0X3 (+2)	78 kDa		0	0	4
Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=1	F8VZY9 (+1)	44 kDa	TRUE	0	0	4
Probable helicase with zinc finger domain OS=Homo sapiens GN=HELZ PE=1 SV=1	J3QS41 (+1)	219 kDa		0	0	4
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	Q86YZ3	282 kDa		0	0	4
Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1	A0A0A0MSX9 (+2)	142 kDa		0	0	4
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=1	E7EUT5 (+2)	28 kDa		0	0	4
Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	P53621 (+1)	138 kDa		0	0	4
Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2	Q99816	44 kDa		0	0	4
Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=1	A0A0A0MRJ6 (+4)	30 kDa		0	0	4
Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3	O95163	150 kDa		0	0	4
Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1	A0A087WVQ6 (+2)	192 kDa		0	0	4
F-box-like/WD repeat-containing protein TBL1XR1 OS=Homo sapiens GN=TBL1XR1 PE=1 SV=1	Q9BZK7	56 kDa		0	0	4
Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=1 SV=1	V9GYM8	116 kDa		0	0	4
26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	O43242	61 kDa		0	0	4
Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	Q9Y446 (+1)	87 kDa		0	0	4
Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	P14868 (+1)	57 kDa		0	0	4
Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	P23246	76 kDa	TRUE	0	0	4
Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2	P35606 (+1)	102 kDa		0	0	4
Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1 PE=1 SV=3	Q86X55 (+1)	66 kDa		0	0	4
Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=2	Q9NZI8	63 kDa	TRUE	0	0	4
Skin-specific protein 32 OS=Homo sapiens GN=XP32 PE=1 SV=1	Q5T750	26 kDa		0	2	3
Isoform 2 of Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2	P62316-2	12 kDa		0	1	3
E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=2	P22681	100 kDa	TRUE	0	0	3
Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	P51659	80 kDa		0	0	3
RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	Q9Y230	51 kDa		0	0	3
Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2	P16402	22 kDa		0	0	3
60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	P10809	61 kDa		0	0	3
Spectrin alpha chain, erythrocytic 1 OS=Homo sapiens GN=SPTA1 PE=1 SV=1	A0A087WZE4 (+2)	281 kDa		0	0	3
Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	P05109	11 kDa		0	0	3
Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=1	G5EA31 (+1)	112 kDa		0	0	3
Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=1	E7EX59	62 kDa		0	0	3
DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	P31689	45 kDa	TRUE	0	0	3
RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	Q96PK6	69 kDa		0	0	3
Signal transducer and activator of transcription OS=Homo sapiens GN=STAT5A PE=1 SV=1	K7EK35 (+2)	87 kDa		0	0	3
Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	P04792	23 kDa		0	0	3
Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=1	A0A0A0MRV0 (+2)	152 kDa		0	0	3
COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=1	A0A096LP07 (+6)	55 kDa		0	0	3
Gephyrin OS=Homo sapiens GN=GPHN PE=1 SV=1	Q9NQX3 (+1)	80 kDa		0	0	3
ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=1	A0A087X2G1 (+3)	74 kDa		0	0	3
Peroxisome assembly factor 2 OS=Homo sapiens GN=PEX6 PE=1 SV=2	Q13608	104 kDa		0	0	3
Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1	Q9ULV4 (+2)	53 kDa		0	0	3
Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	Q6KB66 (+2)	51 kDa	TRUE	0	0	3
Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2	Q9UHD8 (+3)	65 kDa		0	0	3
Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1	P55795	49 kDa	TRUE	0	0	3
Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	P41091	51 kDa		0	0	3
Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	P21333 (+3)	281 kDa	TRUE	0	0	3
CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2	P17812	67 kDa		0	0	3
Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=1 SV=1	J3KPS3 (+2)	40 kDa		0	0	3
E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=1 SV=1	P19474	54 kDa		0	0	3
NEDD8 ultimate buster 1 OS=Homo sapiens GN=NUB1 PE=1 SV=1	H3BM14 (+3)	72 kDa		0	0	3
Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4	Q14160 (+1)	175 kDa		0	0	3
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	J3KT12 (+4)	39 kDa		0	0	3
Lysophosphatidylcholine acyltransferase 2 OS=Homo sapiens GN=LPCAT2 PE=1 SV=1	Q7L5N7	60 kDa		0	0	3
tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	Q9Y3I0	55 kDa		0	0	3
Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=1	A0A0A0MRA5 (+5)	86 kDa		0	0	3
REST corepressor 1 OS=Homo sapiens GN=RCOR1 PE=1 SV=1	J3KN32 (+1)	53 kDa		0	0	3
Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=3	Q8WVV4 (+1)	68 kDa		0	0	3
Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3	O15143	41 kDa		0	0	3
Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	P22314 (+1)	118 kDa		0	0	3
Phosphatidylinositol 4-kinase alpha OS=Homo sapiens GN=PI4KA PE=1 SV=1	J3KN10 (+1)	237 kDa		0	0	3
Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	P55060 (+2)	110 kDa		0	0	3
Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	P58107	556 kDa	TRUE	0	0	3
Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=1	E7EUU4 (+6)	172 kDa		0	0	3
116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1	Q15029 (+2)	109 kDa	TRUE	0	0	3
Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2	P42166	75 kDa		0	0	3
Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	P37802 (+2)	22 kDa		0	0	3
ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=4 SV=1	A0A0D9SF53 (+6)	81 kDa	TRUE	0	0	3
Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	P02452	139 kDa		4	1	2
26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	P62195	46 kDa		0	1	2
Isoform 2 of Dermcidin OS=Homo sapiens GN=DCD	P81605-2	12 kDa		4	0	2
Multifunctional protein ADE2 (Fragment) OS=Homo sapiens GN=PAICS PE=1 SV=1	E9PBS1 (+2)	46 kDa		1	0	2
DNA-directed RNA polymerase OS=Homo sapiens GN=POLR2B PE=1 SV=2	C9J2Y9 (+2)	133 kDa		0	0	2
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	E9PCA1	57 kDa		0	0	2
Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	Q00325 (+1)	40 kDa		0	0	2
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	P15880	31 kDa		0	0	2
Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	P05089 (+1)	35 kDa		0	0	2
Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2	Q01650	55 kDa		0	0	2
Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=1 SV=2	P52888	79 kDa		0	0	2
Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	P31944	28 kDa		0	0	2
Isoform 3 of Sorting nexin-1 OS=Homo sapiens GN=SNX1	Q13596-3	63 kDa		0	0	2
Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4	Q08188	77 kDa		0	0	2
T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	P40227 (+1)	58 kDa		0	0	2
Isoform 2 of 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11	O00231-2 (+1)	48 kDa		0	0	2
Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1	A0A087WW55 (+5)	27 kDa		0	0	2
14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	P61981	28 kDa	TRUE	0	0	2
Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	Q00839 (+1)	91 kDa		0	0	2
Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	P25311	34 kDa		0	0	2
Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1	Q96P63 (+1)	46 kDa		0	0	2
Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=1 SV=2	O60341 (+1)	93 kDa		0	0	2
L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	P07195	37 kDa		0	0	2
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=1	G5E9X5	48 kDa		0	0	2
Protein PRRC2A OS=Homo sapiens GN=PRRC2A PE=1 SV=3	P48634 (+1)	229 kDa		0	0	2
60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=1	E9PLL6 (+1)	12 kDa		0	0	2
Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	P50454	46 kDa		0	0	2
Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	P49411	50 kDa		0	0	2
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1	A0A0C4DG17 (+3)	33 kDa		0	0	2
RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	Q9Y265 (+1)	50 kDa		0	0	2
Melanoma antigen preferentially expressed in tumors OS=Homo sapiens GN=PRAME PE=1 SV=1	P78395	58 kDa		0	0	2
Isoform 3 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1	Q7L1Q6-3	51 kDa		0	0	2
Dual specificity tyrosine-phosphorylation-regulated kinase 1A OS=Homo sapiens GN=DYRK1A PE=1 SV=2	Q13627 (+4)	86 kDa		0	0	2
Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	O43592	110 kDa		0	0	2
Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2	Q9P2J5 (+1)	134 kDa		0	0	2
Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1	Q9BSJ8 (+1)	123 kDa		0	0	2
Cullin 4B, isoform CRA_e OS=Homo sapiens GN=CUL4B PE=1 SV=1	K4DI93 (+3)	103 kDa	TRUE	0	0	2
Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2	P26196	54 kDa		0	0	2
Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	O14744 (+3)	73 kDa		0	0	2
60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	Q02878	33 kDa		0	0	2
GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=1	F8W9S7 (+6)	157 kDa		0	0	2
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	P62269	18 kDa		0	0	2
Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=1 SV=1	D6RAF8 (+7)	23 kDa		0	0	2
Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	Q15393	136 kDa		0	0	2
Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1	A0A087WZ13 (+2)	78 kDa		0	0	2
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	P62701	30 kDa		0	0	2
Transferrin receptor (P90, CD71), isoform CRA_c OS=Homo sapiens GN=TFRC PE=1 SV=1	G3V0E5 (+1)	76 kDa		0	0	2
RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=4 SV=1	A0A0D9SFL3 (+8)	61 kDa		0	0	2
Signal transducer and activator of transcription OS=Homo sapiens GN=STAT3 PE=1 SV=1	G8JLH9 (+3)	76 kDa		0	0	2
Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	Q96QK1	92 kDa		0	0	2
Isoform 2 of Amyloid beta A4 precursor protein-binding family B member 1 OS=Homo sapiens GN=APBB1	O00213-2	77 kDa		0	0	2
Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=1	H3BUF6 (+8)	113 kDa		0	0	2
Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	Q08554 (+1)	100 kDa		0	0	2
ATP-dependent 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	P17858	85 kDa	TRUE	0	0	2
Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	P07384	82 kDa		0	0	2
Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2	Q9P258	56 kDa		0	0	2
60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1	A0A075B7A0 (+6)	16 kDa		0	0	2
Pyruvate kinase OS=Homo sapiens GN=PKM PE=1 SV=1	B4DNK4 (+5)	50 kDa		0	0	2
60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens GN=RPLP0 PE=1 SV=1	F8VPE8 (+9)	17 kDa		0	0	2
Runt-related transcription factor 1 OS=Homo sapiens GN=RUNX1 PE=1 SV=1	H9KVB1 (+5)	41 kDa		0	0	2
Phospholipase D3 (Fragment) OS=Homo sapiens GN=PLD3 PE=1 SV=1	M0QZI4 (+1)	23 kDa		0	0	2
Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	O95373	120 kDa		0	0	2
Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1	P62314	13 kDa		0	0	2
Genetic suppressor element 1 OS=Homo sapiens GN=GSE1 PE=1 SV=3	Q14687 (+2)	136 kDa		0	0	2
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	P62753	29 kDa		0	0	2
Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	Q12906 (+6)	95 kDa		0	0	2
Band 4.1-like protein 2 (Fragment) OS=Homo sapiens GN=EPB41L2 PE=1 SV=1	H0Y5B0	42 kDa		0	0	2
Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	Q93008 (+1)	292 kDa		0	0	2
26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	O00232 (+1)	53 kDa		0	0	2
Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2	Q15645	49 kDa		0	0	2
40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=1	B5MCT8 (+2)	17 kDa		0	0	2
LanC-like protein 1 (Fragment) OS=Homo sapiens GN=LANCL1 PE=1 SV=1	E9PHS0 (+2)	22 kDa		0	0	2
60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	P26373	24 kDa		0	0	2
Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	P23381 (+1)	53 kDa		0	0	2
ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2	Q96HE7	54 kDa		0	0	2
Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3	P41250	83 kDa		0	0	2
Keratin, type II cuticular Hb6 OS=Homo sapiens GN=KRT86 PE=1 SV=1	O43790	53 kDa	TRUE	0	0	1
Ubiquitin-associated and SH3 domain-containing protein B OS=Homo sapiens GN=UBASH3B PE=1 SV=2	Q8TF42	73 kDa		0	0	1
ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	P05141	33 kDa	TRUE	0	0	1
DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1	O60884	46 kDa		0	0	1
Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	F8W726 (+5)	114 kDa		0	0	1
Dedicator of cytokinesis protein 8 OS=Homo sapiens GN=DOCK8 PE=1 SV=3	Q8NF50 (+1)	239 kDa		0	41	0
Tyrosine-protein kinase Tec OS=Homo sapiens GN=TEC PE=1 SV=2	P42680	74 kDa		0	6	0
Leucine-rich repeat and calponin homology domain-containing protein 4 OS=Homo sapiens GN=LRCH4 PE=1 SV=2	O75427	73 kDa		0	6	0
Phosphatidylinositol N-acetylglucosaminyltransferase subunit A OS=Homo sapiens GN=PIGA PE=1 SV=1	P37287 (+1)	54 kDa		0	5	0
Ornithine decarboxylase antizyme 1 (Fragment) OS=Homo sapiens GN=OAZ1 PE=4 SV=5	K7ERW1	22 kDa		0	2	0
Leucine-rich repeat and calponin homology domain-containing protein 3 OS=Homo sapiens GN=LRCH3 PE=1 SV=1	E9PD99 (+4)	68 kDa		0	2	0
Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 PE=1 SV=1	Q7L5D6	37 kDa		0	1	0
Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	P02461	139 kDa		5	0	0
Gamma-secretase-activating protein OS=Homo sapiens GN=GSAP PE=1 SV=2	A4D1B5 (+2)	98 kDa		3	0	0
Protein TRAJ52 (Fragment) OS=Homo sapiens GN=TRAJ52 PE=4 SV=1	A0A075B6W2	2 kDa		1	0	0

SI Table 2: Total spectrum counts of the proteins identified by mass spectrometry following tandem affinity purification of stable Jurkat and K562 cell lines expressing the bait proteins Mb(Lck_1) or Mb(Lck_3), 1st TAP.

Scaffold: Version: Scaffold_4.4.5
Modification Metadata Set: 1541 modifications
Source: C:\Program Files\Scaffold 4\parameters\unimod.xml
Comment:
Protein Grouping Strategy: Experiment-wide grouping with binary peptide-protein weights
Peptide Thresholds: 95.0% minimum
Protein Thresholds: 99.0% minimum and 2 peptides minimum
Peptide FDR: 0.1% (Decoy)
Protein FDR: 1.6% (Decoy)
GO Annotation Source(s):
Displaying:Total Spectrum Count

Identified Proteins (79)	Accession Number	Molecular Weight	Protein Grouping Ambiguity	Jurkat Mb(Lck_1)	Jurkat Mb(Lck_3)	K562 Mb(Lck_1)	K562 Mb(Lck_3)
Tyrosine-protein kinase Lyn OS=Homo sapiens GN=LYN PE=1 SV=3	P07948	59 kDa	TRUE	1	1	112	53
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	P04264	66 kDa	TRUE	56	31	138	46
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	P35527	62 kDa	TRUE	46	37	91	42
ML1_Nadine_Schmit_151201	ML1	18 kDa	TRUE	6	0	54	31
MC2_Nadine_Schmit_151201	MC2	19 kDa	TRUE	5	11	49	28
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	P35908	65 kDa	TRUE	33	32	95	27
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	P13645	59 kDa	TRUE	27	20	89	19
Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	P38646	74 kDa	TRUE	0	0	41	14
Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	P02533	52 kDa	TRUE	13	0	88	11
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	Q9Y490	270 kDa		0	0	12	7
Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	P81605 (+1)	11 kDa		6	0	9	7
CUB domain-containing protein 1 OS=Homo sapiens GN=CDCP1 PE=1 SV=3	Q9H5V8	93 kDa		0	0	31	6
Ubiquitin-40S ribosomal protein S27a (Fragment) OS=Homo sapiens GN=RPS27A PE=1 SV=1	J3QTR3	12 kDa	TRUE	0	1	18	5
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	F5H5D3 (+1)	58 kDa		7	4	9	4
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	P15924	332 kDa		6	1	6	4
Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2	Q8TF72	217 kDa		3	0	3	4
Diacylglycerol kinase theta OS=Homo sapiens GN=DGKQ PE=1 SV=2	P52824	101 kDa		0	0	0	4
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	P11142	71 kDa	TRUE	1	1	54	3
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	P07437	50 kDa	TRUE	5	2	9	3
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	P14923	82 kDa		1	0	3	3
DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	P78527	469 kDa		4	0	44	2
Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	P08107	?	TRUE	0	0	6	2
Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	Q01469	15 kDa		0	0	2	2
Protocadherin alpha-C1 OS=Homo sapiens GN=PCDHAC1 PE=2 SV=2	Q9H158 (+1)	104 kDa		0	0	0	2
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	P08238	83 kDa	TRUE	1	1	17	1
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (Fragment) OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	H7C5W9 (+2)	103 kDa		2	0	5	1
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	P49327	273 kDa		0	0	5	1
Cornifin-B OS=Homo sapiens GN=SPRR1B PE=1 SV=2	P22528 (+1)	10 kDa		1	0	3	1
Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2	Q13085 (+3)	266 kDa	TRUE	0	0	2	1
Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens GN=ATP1A2 PE=1 SV=1	B1AKY9	111 kDa		5	5	0	1
Titin OS=Homo sapiens GN=TTN PE=1 SV=1	A0A0A0MTS7-DECOY (+1)	?	TRUE	0	0	0	1
Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	P08779	51 kDa	TRUE	13	0	98	0
Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	P02538	60 kDa	TRUE	0	0	72	0
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	P13647	62 kDa	TRUE	0	0	55	0
Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	Q04695	48 kDa	TRUE	6	0	41	0
Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=1	K7ERE3 (+2)	45 kDa	TRUE	0	0	28	0
Keratin, type II cuticular Hb6 OS=Homo sapiens GN=KRT86 PE=1 SV=1	O43790	53 kDa	TRUE	0	0	25	0
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	P07900 (+1)	85 kDa	TRUE	1	4	23	0
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	P11021	72 kDa	TRUE	0	0	19	0
Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	P19013	57 kDa	TRUE	0	0	18	0
CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1	F8VPD4 (+1)	236 kDa		2	0	16	0
Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1	P78386	56 kDa	TRUE	0	0	15	0
Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	Q86Y46	59 kDa	TRUE	0	0	14	0
Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2	P34931	70 kDa	TRUE	0	0	14	0
Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	P07814	171 kDa		1	0	9	0
Large proline-rich protein BAG6 OS=Homo sapiens GN=BAG6 PE=1 SV=2	P46379 (+2)	119 kDa		0	0	8	0
Tyrosine-protein kinase Lck OS=Homo sapiens GN=LCK PE=1 SV=6	P06239 (+1)	58 kDa	TRUE	114	109	7	0
Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1	A0A087WVQ6 (+2)	192 kDa		0	0	7	0
Keratin, type I cuticular Ha1 OS=Homo sapiens GN=KRT31 PE=1 SV=3	Q15323	47 kDa	TRUE	0	0	7	0
Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	P05787 (+1)	54 kDa	TRUE	0	0	6	0
Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	Q92616	293 kDa		0	1	4	0
Small proline-rich protein 3 (Fragment) OS=Homo sapiens GN=SPRR3 PE=1 SV=5	B1AN48 (+1)	17 kDa		0	0	3	0
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=1	B0YJC4 (+1)	50 kDa	TRUE	0	0	3	0
Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=1 SV=4	Q92974 (+3)	112 kDa		0	0	3	0
Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	P42704	158 kDa		0	0	3	0
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	Q86YZ3	282 kDa		1	3	2	0
Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1	A0A0C4DGB6 (+4)	69 kDa		2	0	2	0
Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	P55060 (+2)	110 kDa		1	0	2	0
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	P19338	77 kDa		0	0	2	0
Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	P40939	83 kDa		0	0	2	0
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=1	E9PL09 (+3)	25 kDa		0	0	2	0
Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	Q02413	114 kDa		0	0	2	0
Probable helicase with zinc finger domain OS=Homo sapiens GN=HELZ PE=1 SV=1	J3QS41 (+1)	219 kDa		0	0	2	0
Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=1	A0A087WYY6 (+1)	81 kDa		0	0	2	0
Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	Q13263 (+1)	89 kDa		0	3	1	0
Fanconi anemia group D2 protein OS=Homo sapiens GN=FANCD2 PE=1 SV=2	Q9BXW9	164 kDa		1	2	1	0
E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	Q7Z6Z7 (+2)	482 kDa		0	0	1	0
Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1	O95831 (+1)	67 kDa		0	0	1	0
Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	Q5D862	248 kDa		0	0	1	0
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	P13639	95 kDa		0	0	1	0
Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	J3KTA4 (+2)	69 kDa		0	0	1	0
ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=4 SV=1	A0A0D9SF53 (+4)	81 kDa		0	0	1	0
Protein unc-119 homolog A OS=Homo sapiens GN=UNC119 PE=1 SV=1	Q13432	27 kDa		7	10	0	0
E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=2	P22681	100 kDa	TRUE	0	8	0	0
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	P50991 (+1)	58 kDa		1	4	0	0
Protein unc-119 homolog B OS=Homo sapiens GN=UNC119B PE=1 SV=1	A6NIH7	28 kDa		0	4	0	0
Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1	Q29RF7	151 kDa		0	4	0	0
60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	P10809	61 kDa		0	1	0	0
Doublecortin domain-containing protein 1 OS=Homo sapiens GN=DCDC1 PE=4 SV=1	M0R2J8	201 kDa		1	0	0	0

SI Table 3: Total spectrum counts of the proteins identified by mass spectrometry following tandem affinity purification of stable Jurkat and K562 cell lines expressing the bait proteins Mb(Lck_1) or Mb(Lck_3), 2nd TAP.